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## SEQUENCE LISTING

&lt;110&gt; KaloBios, Inc.

&lt;120&gt; TRANSACTIVATION SYSTEM FOR MAMMALIAN CELLS

&lt;130&gt; CELA001/01WO

&lt;160&gt; 23

&lt;170&gt; PatentIn version 3.2

&lt;210&gt; 1

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; hamster

&lt;400&gt; 1

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Phe Ser Phe Gln Pro Glu Ser Asn Pro Thr Pro Ala Val His Arg Asp  
 50 55 60

Met Ala Ala Arg Thr Ser Pro Leu Arg Pro Ile Val Ala Thr Thr Gly  
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Pro Thr Leu Ser Pro Val Pro Pro Val Val His Leu Thr Leu Arg Arg  
 85 90 95

Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Arg Asp Phe Ala Glu Met  
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Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly Arg Phe Ala  
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Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu Ser Val Asn  
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Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro  
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Ser Val Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu  
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Gly His Lys  
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Pro

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Met Ser Phe Thr Leu Leu Ser Tyr Arg Lys Thr Tyr Glu Ile Ser Val  
115 120 125

His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val  
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Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala  
145 150 155 160

Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln  
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Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys  
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Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met  
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Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp  
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Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys  
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Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly  
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Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg  
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Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val  
275 280 285

Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly  
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Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg  
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Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser  
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Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu  
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Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser  
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Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser  
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Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys  
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Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg  
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Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu  
 660 665 670

His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu  
 675 680 685

Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met  
 690 695 700

Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys  
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Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln  
 725 730 735

Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile  
 740 745 750

Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile  
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Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His  
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gccaatgcag cagccactca gccgggtact accattctac agtatgcaca gaccactgat 660  
ggacagcaga tcttagtgcc cagcaaccaa gttgttggtc aagctgcctc tggagacgta 720  
caaacatacc agattcgcac agcaccact agcactattg cccctggagt tgttatggca 780  
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<400> 21

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Ile Ala Thr Leu Ala Gln Val Ser Met Pro Ala Ala His Ala Thr Ser  
35 40 45

Ser Ala Pro Thr Val Thr Leu Val Gln Leu Pro Asn Gly Gln Thr Val  
50 55 60

Gln Val His Gly Val Ile Gln Ala Ala Gln Pro Ser Val Ile Gln Ser  
65 70 75 80

Pro Gln Val Gln Thr Val Gln Ile Ser Thr Ile Ala Glu Ser Glu Asp  
85 90 95

Ser Gln Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg Arg Ile  
100 105 110

Leu Ser Arg Arg Pro Ser Phe Arg Lys Ile Leu Asn Asp Leu Ser Ser  
115 120 125



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<210> 23

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<212> DNA

<213> Artificial

<220>

<223> primer

<400> 23

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30

Primer 14: GTCAAGCAAGCTTGCCGCCACCATGAGACATATTATCTGCCACGG  
(SEQ ID NO: 24)

Primer 15: CGCAGTCTCGAGTTATGGCCTGGGGCGTTTACAGCTC (SEQ ID NO:  
25)

Primer 16: CACCTACCCTTCACGAACTGCATGATTTAGACGTGACGGCC (SEQ ID  
NO: 26)

Primer 17: GGCCGTCACGTCTAAATCATGCAGTTCGTGAAGGGTAGGTG (SEQ ID  
NO: 27)

Primer 18: CGGAGGTGATCGATCTTACCGGCCACGAGGCTGGCTTCCAC (SEQ  
ID NO: 28)

Primer 19: GTGGAAAGCCAGCCTCGTGGCCGGTAAGATCGATCACCTCCG (SEQ  
ID NO: 29)

Primer 20: GTCAAGCAAGCTTGCCGCCACCATGACCATGGAATCTGGAGC (SEQ  
ID NO: 30)

Primer 21: CGCAGTGGATCCTTAATCTGATTTGTGGCAGTAAAGG (SEQ ID NO:  
31)

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 351 gccaaacctt gtaccggagg tgatgatct tacctgccac gaggtggct  
 M P N L V P E V I D L T C H E A G  
 401 ttccaccag tgacgacgag gatgaagagg gtgaggagt ttgttagat  
 F P P S D D E D E E G E E F V L D  
 451 tatgtggagc accccgggca cggttgcagg tctgtcatt atcaccggag  
 Y V E H P G H G C R S C H Y H R  
 501 gaatacgggg gaccagata ttatgtgttc gctttgctat atgaggacct  
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 551 gtggcatgtt tctctacagt cctgtgtctg aacctgagcc tgagcccgag  
 C G M F V Y S P V S E P E P E P E  
 601 ccagaaccgg agcctgcaag acctaccgc cgtcctaaaa tggcgccctgc  
 P E P E P A R P T R R P K M A P  
 651 tatctgaga cgcccgacat cacctgtgtc tagagaatgc aatagtagta  
 A I L R R P T S P V S R E C N S S  
 701 cggatagctg tgactccggt ccttctaaca cacctcctga gataccccg  
 T D S C D S G P S N T P P E I H P  
 751 gtggtccgc tgtgccccat taaaccagtt gccgtgagag ttggtgggcg  
 V V P L C P I K P V A V R V G G  
 801 tcgccaggct gtggaatgta tcgaggactt gcttaacgag cctgggcaac  
 R R Q A V E C I E D L L N E P G Q  
 851 ctttggactt gagctgtaaa cgccccaggc cataactcga g  
 P L D L S C K R P R P - *XhoI*

(From Figure 11) Nucleotide coding sequence of E1A mutant  
 Y47H (SEQ ID NO: 41):

1 aagcttgccg ccaccatgag acatattatc tgccacggag gtgttattac  
*HindIII* M R H I I C H G G V I  
 51 cgaagaaatg gccgccagtc tttggacca gctgatcgaa gaggtactgg  
 T E M A A S L L D Q L I E E V L  
 101 ctgataatct tccacctcct agccattttg aaccacctac ctttcacgaa  
 A D N L P P P S H F E P P T L H E  
 151 ctgcatgatt tagacgtgac ggcccccgaa gatcccaacy aggaggcggt  
 L H D L D V T A P E D P N E E A  
 201 ttgcagatt ttcccgact ctgtaatgtt gccggtgcag gaagggattg  
 V S Q I F P D S V M L A V Q E G I  
 251 acttactcac tttccgccc gcccccgggt ctccggagcc gcctcacctt  
 D L L T F P P A P G S P E P P H L  
 301 tcccggcagc ccgagcagcc ggagcagaga gccttgggtc cggtttctat  
 S R Q P E Q P E Q R A L G P V S  
 351 gccaaacctt gtaccggagg tgatgatct tacctgccac gaggtggct

S R R P S Y R K I L N D L S S D A  
 451 ccaggggtgc caaggattga agaagaaaag tcggaagagg agacttcagc  
 P G V P R I E E E K S E E E T S  
 501 ccctgccatc accactgtga cagtgccaac tccgatttac cagacaagca  
 A P A I T T V T V P T P I Y Q T S  
 551 gtgggcagta tattgccatt acccagggag gagctataca gctggctaac  
 S G Q Y I A I T Q G G A I Q L A N  
 601 aatggtagcg atgggttaca gggccttcag acattaacca tgaccaatgc  
 N G T D G V Q G L Q T L T M T N  
 651 agctgccact cagccgggta ccactattct acagtatgca cagaccactg  
 A A A T Q P G T T I L Q Y A Q T T  
 701 atggacagca gattctagtg cccagcaacc aagtgttgt tcaagctgcc  
 D G Q Q I L V P S N Q V V V Q A A  
 751 tctggcgatg tacaacata ccaattcgt acagcaccca ctagcaccat  
 S G D V Q T Y Q I R T A P T S T  
 801 cgccccctga gtgttatgg catcctcccc agcacttctt acgcagcctg  
 I A P G V V M A S S P A L P T Q P  
 851 ctgaagaagc agcccggag agagaggttc gtctaataaa gaacagggaa  
 A E E A A R K R E V R L M K N R E  
 901 gcagcaagag aatgtcgtag aaagaagaaa gaatatgtga aatgtttaga  
 A A R E C R R K K K E Y V K C L  
 951 gaacagagtg gcagtgcctg aaaacaaaaa caagacattg attgaggagc  
 E N R V A V L E N Q N K T L I E E  
 1001 taaaagcact taaggacctt tactgccaca aatcagatta aggatcc  
 L K A L K D L Y C H K S D - *Bam*HI

(From Figure 13) Nucleotide coding sequence of hamster CREB-  
 B mutant Y134F (SEQ ID NO: 43):

1 aagcttgccg ccaccatgac catggaatct ggagcagaca accagcagag  
 HindIII M T M E S G A D N Q Q  
 51 tggagatgct gctgtaacag aagctgaaaa tcaacaaatg acagctcaag  
 S G D A A V T E A E N Q Q M T A Q  
 101 cccaaccaca gattgccaca ttagcccagg tatccatgcc agcagctcat  
 A Q P Q I A T L A Q V S M P A A H  
 151 gcgacatcat ctgctccac tgaacctta gtgcagctgc ccaatgggca  
 A T S S A P T V T L V Q L P N G  
 201 gacagtccaa gtccatggag ttattcaggc ggcccagcca tcagttattc  
 Q T V Q V H G V I Q A A Q P S V I  
 251 agtctccaca agtccaaaca gttcagttct cctgtaagga cttaaaaaga  
 Q S P Q V Q T V Q S S C K D L K R  
 301 cttttctccg gaactcagat ttaactatt gcagaaagtg aggattcaca  
 L F S G T Q I S T I A E S E D S

201 tggtagctg ttgattctt tgaatctggg tcaccaggcg cttttcaag  
 C G E L F D S L N L G H Q A L F Q  
 251 agaaggtcat caagactttg gatttttcca caccggggcg cgctgcggct  
 E K V I K T L D F S T P G R A A A  
 301 gctgttgctt tttgagttt tataaaggat aaatggagcg aagaaacca  
 A V A F L S F I K D K W S E E T  
 351 tctgagcggg gggtagctgc tggattttct ggccatgcat ctgtggagag  
 H L S G G Y L L D F L A M H L W R  
 401 cggttgtgag acacaagaat cgcctgctac tgtgtcttc cgtccgccc  
 A V V R H K N R L L L L S S V R P  
 451 gcgataatac cgacggagga gcagcagcag cagcaggagg aagccaggcg  
 A I I P T E E Q Q Q Q Q E E A R  
 501 gcggcggcag gagcagagcc catggaaccc gagagccggc ctggaccctc  
 R R R Q E Q S P W N P R A G L D P  
 551 gggaatgac taga  
 R E - *XbaI*

(From Figure 15) Nucleotide coding sequence of hamster Bcl2 deletion mutant (SEQ ID NO: 45):

*NcoI*  
 1 ccatggctca agctgggaga acagggatg ataaccgaga gatcgtgatg  
 M A Q A G R T G Y D N R E I V M  
 51 aagtacatcc attataagct gtcacagagg ggctacgagt gggatgtggg  
 K Y I H Y K L S Q R G Y E W D V  
 101 agatgtggac gccgcggccg cggccgcgag ccccggtcca cctgtggtcc  
 G D V D A A A A A A S P V P P V V  
 151 acctgaccct ccgcccgggt ggggatgact tctcccgtcg ctaccgtcgc  
 H L T L R R A G D D F S R R Y R R  
 201 gacttcgagg agatgtccag tcagctgcac ctgacgccct tcaccgcgag  
 D F A E M S S Q L H L T P F T A  
 251 gggacgctt gctacggtgg tggaggaact cttcaggat ggggtgaact  
 R G R F A T V V E E L F R D G V N  
 301 gggggaggat tgtggccttc ttgagttcg gtggggtcat gtgtgtggag  
 W G R I V A F F E F G G V M C V E  
 351 agcgtcaaca gggagatgtc acccctgggt gacaacatcg ccctgtggat